

FIGURE 1

Page 1

FIGURE 2A

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FIGURE 2A

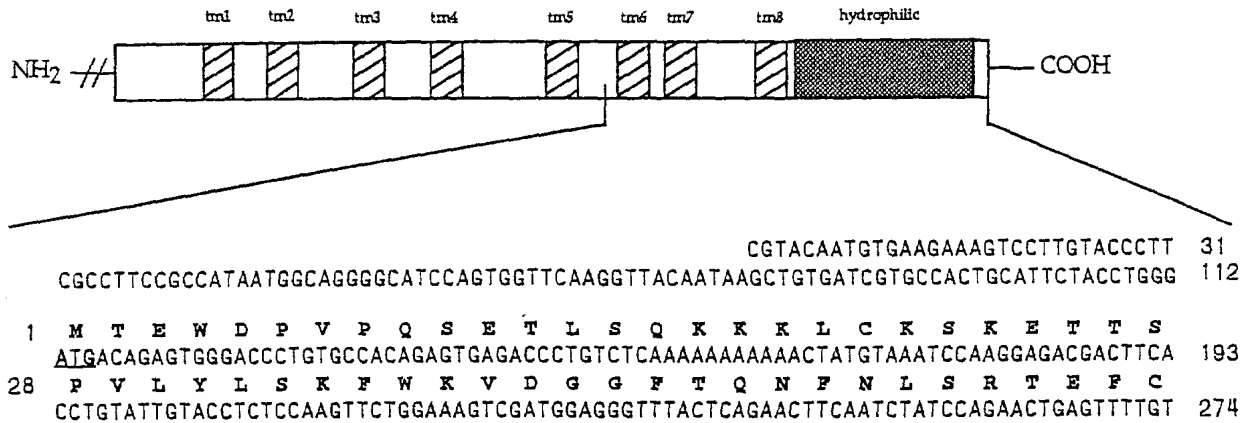
[illegible]

Translation of full length pmt cDNA

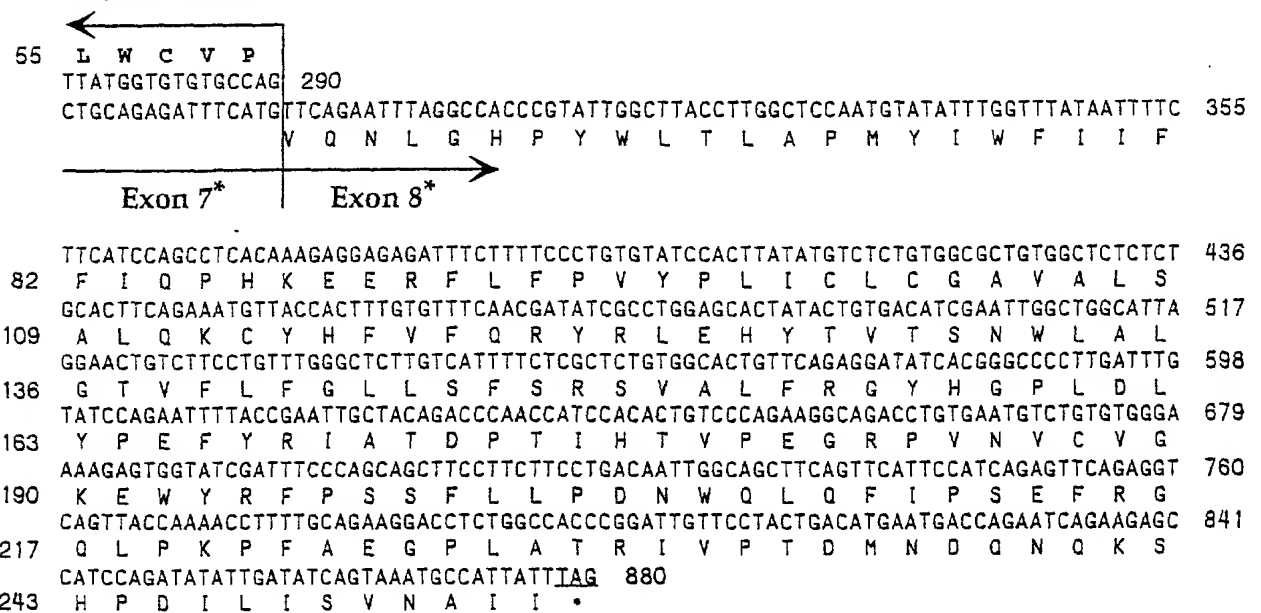
1	MASRGARQRL	KGSGASSGDT	APAADKLREL	LGSREAGGAE	HRTELSGNKA
51	GQVWAPEGST	AFKCLLSARL	CAALLSNISD	CDETFNYWEP	THYLIYGEGF
101	QTWEYSPAYA	IRSYAYLLLH	AWPAAFHARI	LQTNKILVfy	FLRCLLAFVS
151	CICELYFYKA	VCKKFGLHVS	RMMLAFLVLS	TGMFCSSSAF	LPSSFECMYTT
201	LIAMTGWYMD	KTSIAVLGVA	AGAILGWPFs	AALGLPIAFD	LLVMKHRWKS
251	FFHWSLMALI	LELVFVVVID	SYYYGKLVIA	PLNIVLYNVF	TPHGPDLYGT
301	EPWYFYLING	FLNFNVAFAL	ALLVLPLTSL	MEYLLQRFHV	QNLGHPYWLT
351	LAPMYIWFII	FFIQPHKEER	FLFPVYPLIC	LCGAVALSAL	QKCYHFVFQR
401	YRLEHYTVTS	NWLALGTVFL	FGLLSFSRSV	ALFRGYHGPL	DLYPEFYRIA
451	TDPTIHTVPE	GRPVNVCVGK	EWYRFPSSFL	LPDNWQLQFI	PSEFRGQLPK
501	PFAEGPLATR	IVPTDMNDQN	LEEPSRYIDI	SKCHYLVLDL	TMRETPREPCK
551	YSSNKEEWIS	LAYRPFLDAS	RSSKLLRAFY	VPFLSDQYTV	YVNYTILKPR
601	KAKQIRKKSG	G			

Schematic of Fusion Open Reading Frame

putative Mannose Transferase



Fusion Partner



Partner - putative Mannose Transferase fusion

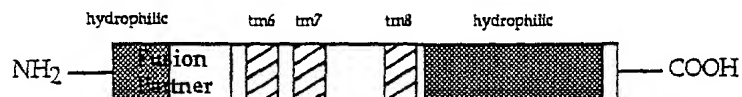


FIGURE 3

PUTATIVE MANNOSYL TRANSFERASE 5'-FUSION TRANSCRIPT

CGTACAATGTGAAGAAAGTCCTTGTACCCCTTCGCTTCCGCCATAATGGCAGGGGCATCCAGTGGTTCAAGGTTACAATA

AGCTGTGATCGTGCCACTGCATTCTAOCCTGGGATGACAGAGTGGGAOCCTGTGCCACAGAGTGAGACOCCTGTCTCAAAAA

M T E W D P V P Q S E T L S Q K

AAAAAACTATGTAAATCCAAGGAGACGACTTCACCTGTATTGTACCTCTCCAAGTTCTGGAAAGTCGATGGAGGGTTTAC

K K L C K S K E T T S P V L Y L S K F W K V D G G F T

CAGAACTTCAATCTATCCAGAACTGAGTTTTGTTTTATGGTGTGTGCCAGTTCAGAATTTAGGCCACCCGTTATTGGCTTA

Q N F N L S R T E F C L W C V P

CCTTGGCTCCAATGTATATTTGGTTTATAATTTCTTCATCCAGCCTCACAAAGAGGAGAGATTTCTTTTCCCTGTGTAT
CCACTTATATGTCTCTGTGGCGCTGTGGCTCTCTCTGCACTTCAGAAATGTTACCACTTTGTGTTTCAAOGATATOGCT
GGAGCACTATACTGTGACATCGAATTGGCTGGCATTAGGAACTGTCTTCTGTTTGGGCTCTTGTCAATTTCTOGCTCTG
TGGCACTGTTTCAGAGGATATCACGGGCCCCCTTGATTTGTATCCAGAATTTTACCGAATTGCTACAGACCCCAACCATOCAC
ACTGTCCAGAAGGCAGACCTGTGAATGTCTGTGTGGGAAAAGAGTGGTATOGATTTCCAGCAGCTTCTCTTCTCTGA
CAATTGGCAGCTTCAGTTCATTTCATCAGAGTTCAGAGGTTCAGTTACCAAAACCTTTTGCAGAAGGACCTCTGGCCACCC
GGATTGTTCTACTGACATGAATGACCAGAATCAGAAGAGCCATCCAGATATATTGATATCAGTAAATGCCATTATTTAG
TGGATTTGGACAOCATGAGAGAAACACCCCGGGAGCCAAAATATTCATCCAATAAAGAAGAATGGATCAGCTTGGCCTAT
AGACCATTCCTTGATGCTTCTAGATCTTCAAAGCTGCTGCGGGCATTCTATGTCCCTTCTCTGTGATCAGTATACAGT
GTACGTAAACTACAOCATCCTCAAACCCCGGAAAGCAAAGCAAATCAGGAAGAAAAGTGGAGGTTAGCAACACAOCCTGTG
GCCCCAAAGGACAACCATCTTGTTAACTATTGATTCCAGTGACCTGACTCCCTGCAAGTCATOGCTGTAAACATTGTAA
AAAGGTCTTCTGACATGAAAAAAAAA

FIGURE 4

Putative Fusion protein chr 11/9

```

      NcoI
      ~~~~~
1      Met AlaSerArg GlyAlaArg GlnArgLeuLys GlySerGly·
      A TGGCTAGTCG AGGGGCTCGG CAGCGCCTGA AGGGCAGCGG
      T ACCGATCAGC TCCCCGAGCC GTCGCGGACT TCCCGTCGCG
      ~~~~~
51      ·AlaSerSer GlyAspThrAla ProAlaAla AspLysLeu ArgGluLeuLeu·
      GGCCAGCAGT GGGGATACGG CCCC GGCTGC GGACAAGCTG CGGGAGCTGC
      CCGGTCGTCA CCCCTATGCC GGGGCCGACG CCTGTTCGAC GCCCTCGACG
      ~~~~~
101     ·LGlySerArg GluAlaGly GlyAlaGluHis ArgThrGlu LeuSerGly
      TGGGCAGCCG AGAGGCGGGC GCGCGGAGC ACCGGACCGA GTTATCTGGG
      ACCCGTCGGC TCTCCGCCCG CCGCGCCTCG TGGCCTGGCT CAATAGACCC
      ~~~~~
151     AsnLysAlaGly GlnValTrp AlaProGlu GlySerThrAla PheLysCys·
      AACAAAGCAG GACAAGTCTG GGCACCTGAA GGATCTACTG CTTTCAAGTG
      TTGTTTCGTC CTGTTCAGAC CCGTGGACTT CCTAGATGAC GAAAGTTCAC
      ~~~~~
201     ·LeuLeuSer AlaArgLeuCys AlaAlaLeu LeuSerAsn IleSerAspCys·
      TCTGCTTTCA GCAAGGTTAT GTGCTGCTCT CCTGAGCAAC ATCTCTGACT
      AGACGAAAGT CGTTCCAATA CACGACGAGA GGACTCGTTG TAGAGACTGA
      ~~~~~
251     ·CAspGluThr PheAsnTyr TrpGluProThr HisTyrLeu IleTyrGly
      GTGATGAAAC ATTCAACTAC TGGGAGCAA CACACTACCT CATCTATGGG
      CACTACTTTG TAAGTTGATG ACCCTCGGTT GTGTGATGGA GTAGATACCC
      ~~~~~
301     GluGlyPheGln ThrTrpGlu TyrSerPro AlaTyrAlaIle ArgSerTyr·
      GAAGGGTTTC AGACTTGGA ATATTCCCA GCATATGCCA TTCGCTCCTA
      CTTCCCAAAG TCTGAACCCT TATAAGGGGT CGTATACGGT AAGCGAGGAT
      ~~~~~
      EcoRI
      ~~~~~
351     ·AlaTyrLeu LeuLeuHisAla TrpProAla AlaPheHis AlaArgIleLeu·
      TGCTTACCTG TTGCTTCATG CCTGGCCAGC TGCATTTTCAT GCAAGAATTC
      ACGAATGGAC AACGAAGTAC GGACCGGTCG ACGTAAAGTA CGTTCTTAAG
      ~~~~~
401     ·LGlnThrAsn LysIleLeu ValPheTyrPhe LeuArgCys LeuLeuAla
      TACAAACTAA TAAGATTCTT GTGTTTTACT TTTTGCGATG TCTTCTGGCT
      ATGTTTGATT ATTCTAAGAA CACAAAATGA AAAACGCTAC AGAAGACCGA
      ~~~~~
451     PheValSerCys IleCysGlu LeuTyrPhe TyrLysAlaVal CysLysLys·
      TTTGTGAGCT GTATTTGTGA ACTTTACTTT TACAAGGCTG TGTGCAAGAA
      AAACACTCGA CATAAACAAT TGAAATGAAA ATGTTCCGAC ACACGTTCTT
      ~~~~~
501     ·PheGlyLeu HisValSerArg MetMetLeu AlaPheLeu ValLeuSerThr·
      GTTTGGGTTG CACGTGAGTC GAATGATGCT AGCCTTCTTG GTTCTCAGCA
      CAAACCCAAC GTGCACTCAG CTTACTACGA TCGGAAGAAC CAAGAGTCGT

```

FIGURE 5


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~~~~~
551  •TGLyMetPhe CysSerSer SerAlaPheLeu ProSerSer PheCysMet
    CTGGCATGTT TTGCTCATCA TCAGCATTCC TTCCTAGTAG CTTCTGTATG
    GACCGTACAA AACGAGTAGT AGTCGTAAGG AAGGATCATC GAAGACATAC
    ~~~~~
601  TyrThrThrLeu IleAlaMet ThrGlyTrp TyrMetAspLys ThrSerIle•
    TACACTACGT TGATAGCCAT GACTGGATGG TATATGGACA AGACTTCCAT
    ATGTGATGCA ACTATCGGTA CTGACCTACC ATATACCTGT TCTGAAGGTA
    ~~~~~
651  •AlaValLeu GlyValAlaAla GlyAlaIle LeuGlyTrp ProPheSerAla•
    TGCTGTGCTG GGAGTAGCAG CTGGGGCTAT CTTAGGCTGG CCATTCACTG
    ACGACACGAC CCTCATCGTC GACCCCGATA GAATCCGACC GGTAAGTCAC
    ~~~~~
701  •AAlaLeuGly LeuProIle AlaPheAspLeu LeuValMet LysHisArg
    CAGCTCTTGG TTTACCCATT GCCTTTGATT TGCTGGTCAT GAAACACAGG
    GTCGAGAACC AAATGGGTAA CGGAAACTAA ACGACCAGTA CTTTGTGTCC
    ~~~~~
751  TrpLysSerPhe PheHisTrp SerLeuMet AlaLeuIleLeu PheLeuVal•
    TGGAAGAGTT TCTTTCATTG GTCGCTGATG GCCCTCATAC TATTTCTGGT
    ACCTTCTCAA AGAAAGTAAC CAGCGACTAC CGGGAGTATG ATAAAGACCA
    •ProValVal ValIleAspSer TyrTyrTyr GlyLysLeu ValIleAlaPro•
801  GCCTGTGGTG GTCATTGACA GCTACTATTA TGGGAAGTTG GTGATTGCAC
    CGGACACCAC CAGTAACTGT CGATGATAAT ACCCTTCAAC CACTAACGTG
    •PLeuAsnIle ValLeuTyr AsnValPheThr ProHisGly ProAspLeu
851  CACTCAACAT TGTTTTGTAT AATGTCTTTA CTCCTCATGG ACCTGATCTT
    GTGAGTTGTA ACAAACATA TTACAGAAAT GAGGAGTACC TGGACTAGAA
    TyrGlyThrGlu ProTrpTyr PheTyrLeu IleAsnGlyPhe LeuAsnPhe•
901  TATGGTACAG AACCCTGGTA TTTCTATTTA ATTAATGGAT TTCTGAATTT
    ATACCATGTC TTGGGACCAT AAAGATAAAT TAATTACCTA AAGACTTAAA
    •AsnValAla PheAlaLeuAla LeuLeuVal LeuProLeu ThrSerLeuMet•
951  CAATGTAGCC TTTGCTTTGG CTCTCCTAGT CCTACCACTG ACTTCTCTTA
    GTTACATCGG AAACGAAACC GAGAGGATCA GGATGGTGAC TGAAGAGAAT
    PstI
    ~~~~~
1001 •MGLuTyrLeu LeuGlnArg PheHis
    TGGAATACCT GCTGCAGAGA TTTCATG
    ACCTTATGGA CGACGTCTCT AAAGTAC

```

FIGURE 5

Putative fusion protein 9/11

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1   CGTACAATGT GAAGAAAGTC CTTGTACCCT TCGCCTTCCG CCATAATGGC
   GCATGTTACA CTTCTTTTCAG GAACATGGGA AGCGGAAGGC GGTATTACCG
51  AGGGGCAATC CAGTGGTTCA AGGTTACAAT AAGCTGTGAT CGTGCCACTG
   TCCCCGTTAG GTCACCAAGT TCCAATGTTA TTCGACACTA GCACGGTGAC
       MetThrGlu TrpAspPro ValProGln SerGluThrLeu·
       ~~~~~

101  CATTCTACCT GGGATGACAG AGTGGGACCC TGTGCCACAG AGTGAGACCC
   GTAAGATGGA CCCTACTGTC TCACCCTGGG ACACGGTGTC TCACTCTGGG
   ·LSerGlnLys LysLysLeu CysLysSerLys GluThrThr SerProVal
   ~~~~~

151  TGTCTCAAAA AAAAAAATA TGTAATCCA AGGAGACGAC TTCACCTGTA
   ACAGAGTTTT TTTTTTTGAT ACATTTAGGT TCCTCTGCTG AAGTGGACAT
   LeuTyrLeuSer LysPheTrp LysValAsp GlyGlyPheThr GlnAsnPhe·
   ~~~~~

201  TTGTACCTCT CCAAGTTCTG GAAAGTCGAT GGAGGGTTTA CTCAGAACTT
   AACATGGAGA GGTTCAAGAC CTTTCAGCTA CCTCCCAAAT GAGTCTTGAA
   ·AsnLeuSer ArgThrGluPhe CysLeuTrp CysValPro   GlnAsnLeu·
   ~~~~~

251  CAATCTATCC AGAACTGAGT TTTGTTTATG GTGTGTGCCA GTTCAGAATT
   GTTAGATAGG TCTTGACTCA AAACAAATAC CACACACGGT CAAGTCTTAA
   ·LGlyHisPro TyrTrpLeu ThrLeuAlaPro MetTyrIle TrpPheIle
   ~~~~~

301  TAGGCCACCC GTATTGGCTT ACCTTGGCTC CAATGTATAT TTGGTTTATA
   ATCCGGTGGG CATAACCGAA TGGAAACCGAG GTTACATATA AACCAAATAT
   ~~~~~
   IlePhePheIle GlnProHis LysGluGlu ArgPheLeuPhe ProValTyr·
   ~~~~~

351  ATTTTCTTCA TCCAGCCTCA CAAAGAGGAG AGATTTCTTT TCCCTGTGTA
   TAAAAGAAGT AGGTCGGAGT GTTCTCCTC TCTAAAGAAA AGGGACACAT
   ~~~~~
   ·ProLeuIle CysLeuCysGly AlaValAla LeuSerAla LeuGlnLysCys·
   ~~~~~

401  TCCACTTATA TGTCTCTGTG GCGCTGTGGC TCTCTCTGCA CTTCAGAAAT
   AGGTGAATAT ACAGAGACAC CGCGACACCG AGAGAGACGT GAAGTCTTTA
   ~~~~~
   ·CTyrHisPhe ValPheGln ArgTyrArgLeu GluHisTyr ThrValThr
   ~~~~~

451  GTTACCACTT TGTGTTTCAA CGATATCGCC TGGAGCACTA TACTGTGACA
   CAATGGTGAA ACACAAAGTT GCTATAGCGG ACCTCGTGAT ATGACACTGT
   ~~~~~
   SerAsnTrpLeu AlaLeuGly ThrValPhe LeuPheGlyLeu LeuSerPhe·
   ~~~~~

501  TCGAATTGGC TGGCATTAGG AACTGTCTTC CTGTTTGGGC TCTTGTCATT

```

FIGURE 6

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AGCTTAACCG ACCGTAATCC TTGACAGAAG GACAAACCCG AGAACAGTAA
~~~~~
•SerArgSer ValAlaLeuPhe ArgGlyTyr HisGlyPro LeuAspLeuTyr•
~~~~~
551 TTCTCGCTCT GTGGCACTGT TCAGAGGATA TCACGGGCCC CTTGATTGT
AAGAGCGAGA CACCGTGACA AGTCTCCTAT AGTGCCCGGG GAACTAAACA
~~~~~
•TProGluPhe TyrArgIle AlaThrAspPro ThrIleHis ThrValPro
~~~~~
601 ATCCAGAATT TTACCGAATT GCTACAGACC CAACCATCCA CACTGTCCCA
TAGGTCTTAA AATGGCTTAA CGATGTCTGG GTTGGTAGGT GTGACAGGGT
                               ClaI
                               ~~~~~
GluGlyArgPro ValAsnVal CysValGly LysGluTrpTyr ArgPhePro•
~~~~~
651 GAAGGCAGAC CTGTGAATGT CTGTGTGGGA AAAGAGTGGT ATCGATTTC
CTTCCGTCTG GACACTTACA GACACACCCT TTTCTCACC TAGCTAAAGG
•SerSerPhe LeuLeuProAsp AsnTrpGln LeuGlnPhe IleProSerGlu•
~~~~~
701 CAGCAGCTTC CTTCTTCCTG ACAATTGGCA GCTTCAGTTC ATTCCATCAG
GTCGTCAAG GAAGAAGGAC TGTTAACCGT CGAAGTCAAG TAAGGTAGTC
•GPheArgGly GlnLeuPro LysProPheAla GluGlyPro LeuAlaThr
~~~~~
751 AGTTCAGAGG TCAGTTACCA AAACCTTTTG CAGAAGGACC TCTGGCCACC
TCAAGTCTCC AGTCAATGGT TTTGGAAAC GTCTTCCTGG AGACCGGTGG
ArgIleValPro ThrAspMet AsnAspGln AsnLeuGluGlu ProSerArg•
~~~~~
801 CGGATTGTTC CTACTGACAT GAATGACCAG AATCTAGAAG AGCCATCCAG
GCCTAACAAG GATGACTGTA CTTACTGGTC TTAGATCTTC TCGGTAGGTC
•TyrIleAsp IleSerLysCys HisTyrLeu ValAspLeu AspThrMetArg•
~~~~~
851 ATATATTGAT ATCAGTAAAT GCCATTATT AGTGGATTG GACACCATGA
TATATAACTA TAGTCATTTA CGGTAATAAA TCACCTAAAC CTGTGGTACT
                               SmaI
                               ~~~~~
                               XmaI
                               ~~~~~
                               AvaI
                               ~~~~~
•AGluThrPro ArgGluPro LysTyrSerSer AsnLysGlu GluTrpIle
~~~~~
901 GAGAAACACC CCGGGAGCCA AAATATTCAT CCAATAAAGA AGAATGGATC
CTCTTTGTGG GGCCCTCGGT TTTATAAGTA GGTATTCTCT TCTTACCTAG
SerLeuAlaTyr ArgProPhe LeuAspAla SerArgSerSer LysLeuLeu•
~~~~~
951 AGCTTGGCCT ATAGACCATT CCTTGATGCT TCTAGATCTT CAAAGCTGCT
TCGAACCGGA TATCTGGTAA GGAACACGA AGATCTAGAA GTTTCGACGA
•ArgAlaPhe TyrValProPhe LeuSerAsp GlnTyrThr ValTyrValAsn•
~~~~~
1001 GCGGGCATTTC TATGTCCCCT TCCTGTCAGA TCAGTATACA GTGTACGTAA
CGCCCCGTAAG ATACAGGGGA AGGACAGTCT AGTCATATGT CACATGCATT
•ATyrThrIle LeuLysPro ArgLysAlaLys GlnIleArg LysLysSer

```

FIGURE 6

```
~~~~~  
1051  ACTACACCAT CCTCAAACCC CGGAAAGCAA AGCAAATCAG GAAGAAAAGT  
      TGATGTGGTA GGAGTTTGGG GCCTTTCGTT TCGTTTAGTC CTTCTTTTCA  
      GlyGly  
      ~~~~~  
1101  GGAGGTTAGC AACACACCTG TGGCCCCAAA GGACAACCAT CTTGTAACT  
      CCTCCAATCG TTGTGTGGAC ACCGGGGTTT CCTGTTGGTA GAACAATTGA  
1151  ATTGATTCCA GTGACCTGAC TCCCTGCAAG TCATCGCCTG TAACATTTGT  
      TAACTAAGGT CACTGGACTG AGGGACGTTT AGTAGCGGAC ATTGTAAACA  
1201  AATAAAGGTC TTCTGACATG AAAAA  
      TTATTTCCAG AAGACTGTAC TTTTT
```

FIGURE 6

FIGURE 6

Chromosome 9 est (gene) involved in fusion:

```

1      AGCGGGTGGG CGCGAGTCGG CCTCCCGCGG TGCCGCCGCA GCGTGGCGCG
      TCGCCCACCC GCGCTCAGCC GGAGGGCGCC ACGGCGGCGT CGCACC GCGC
51     GAGAGGCAGG GGCATCCAGT GGTTC AAGGT TACAATAAGC TGTGATCGTG
      CTCTCCGTCC CCGTAGGTCA CCAAGTTCCA ATGTTATTCG ACACTAGCAC
                                           Glu•
                                           ~~~
101    CCACTGCATT CTACCTGGGA TGACAGAGTG GGACCCTGTG CCACAGAGTG
      GGTGACGTAA GATGGACCCT ACTGTCTCAC CCTGGGACAC GGTGTCTCAC
      •GThrLeuSer GlnLysLys LysLysLeuCys LysSerLys LysLysArg
      ~~~~~
151    AGACCCTGTC TCAAAAAAAA AAAAACTAT GTAAATCCAA GAAAAAAGA
      TCTGGGACAG AGTTTTTTTT TTTTGTGATA CATTTAGGTT CTTTTTTTCT
      LysGlnLeuLeu TrpProPhe AlaSerHis ProGluArgVal SerIleGly•
      ~~~~~
201    AAACAGCTCC TGTGGCCTTT TGCCTCTCAT CCAGAAAGGG TATCCATTGG
      TTTGTGCGAGG ACACCGGAAA ACGGAGAGTA GGTCTTTCCC ATAGGTAACC
      •LeuSerAsn IleSerSerSer CysGlnAla ThrAsnGly AspAspProPro•
      ~~~~~
251    CCTTTCTAAT ATCTCTTCAT CCTGTCAGGC CACAAATGGA GACGACCCAC
      GGAAAGATTA TAGAGAAGTA GGACAGTCCG GTGTTTACCT CTGCTGGGTG
      •PValTrpTyr LeuSerLys PheTrpLysVal AspGlyGly PheThrGln
      ~~~~~
301    CTGTATGGTA CCTCTCCAAG TTCTGGAAAG TCGATGGAGG GTTTACTCAG
      GACATACCAT GGAGAGGTTC AAGACCTTTC AGCTACCTCC CAAATGAGTC
      AsnPheAsnLeu SerArgThr GluPheGly LysTrpCysVal ProGlyArg•
      ~~~~~
351    AACTTCAATC TATCCAGAAC TGAGTTTGGT AAATGGTGTG TGCCAGGCAG
      TTGAAGTTAG ATAGGTCTTG ACTCAAACCA TTTACCACAC ACGGTCCGTC
                                           EcoRI
                                           ~~~~~
      •GlyLeuAsn SerSerAlaTyr HisTrpAla GluValThr GlyIleGlnGlu•
      ~~~~~
401    GGGATTAAAC AGTAGTGCAT ATCACTGGGC TGAAGTGACA GGAATTCAAG
      CCCTAATTTG TCATCACGTA TAGTGACCCG ACTTCACTGT CCTTAAGTTC
      •GlnAsnAla SerThrPro ProValSerLeu SerCysLeu PheLeuLeu
451    AACAGAATGC ATCCACTCCT CCAGTCTCAT TAAGCTGCCT CTTTCTACTG
      TTGTCTTACG TAGGTGAGGA GGTCAGAGTA ATTCGACGGA GAAAGATGAC
      LysTrpArgTrp GlyPheGln AspThrSer GlnProThrGly ThrThrGly•
501    AAATGGCGAT GGGGATTCCA GGACACCTCT CAACCTACAG GAACCACTGG
      TTTACCGCTA CCCCTAAGGT CCTGTGGAGA GTTGGATGTC CTTGGTGACC
      •Ser
551    ATCTAA
      TAGATT

```

FIG. 7

FIGURE 7

FIGURE 8. Sequences of mannosyl transferase proteins.

Human (SEQ ID NO: 2) (100%)

1 masrgarqrl kgsqassgdt apaadklrel lgsreaggae hrtelsnka gqvwapegst
61 afkcillsarl caallsnisd cdefnywep thyliyggegf qtweyspaya irsyaylllh
121 awpaafhari lqtnkilvfy flrcllafvs cicelyfyka vckkfghlvs rmmalafvlvs
181 tgmfcsssaf lpssfcmytt liamtgwymd ktsiavlga agailgwpgs aalglpiafd
241 llvmkhrwks ffhwsmlali lflvpvvid syyygklvia plnivlynvf tphgpdlygt
301 epwyfying flnfnvafal allvpltsl meyllqrfhv qnlghpywlt lapmyiwfii
361 ffiqphkeer flfpvyplic lcgavalsal qkcyhfvfqr yrlehytvts nwlalgtvfl
421 fgllsfersv alfrgyhgpl dlypefyria tdptihtvpe grpvnvcvgk ewyrfpssfl
481 lpdnwqlqfi psefrgqlpk pfaegplatr ivptdmndqn leapsryidi skchylvdld
541 tmretprepk yssnkeewis layrpfldas rsskllrafy vpflsdqyvt yvnytilkpr
601 kakqirkksg g

S. cerevisiae (ALG9) (SEQ ID NO:11) (33.1%)

mpskaprksl svsfvwtfsi lavlrtsas frviddcdev ynywepihyl lygyglqtwe
yspeyairsw fyialhavpg flarglglr lhfvyfirgv lacfsafcet nlilavarnf
nravalhlts vlfvnsqmw satsflpssf amnmvtlals aqlspstkr tvkvvsfity
gavigwpfsa alsipfille lvdikgrfhr lfcwfkaf vallitgici tvdslyfhyri
qfvawnivky nvlakdgrgp diygteppwy yfanlsqhn iwlwfamacg plvllaafn
winldsflldl ssvispfyiw lfifliqphk eerfmypiyp vlclaaaigl dmslklmiqi
lssinetvrs kfpvrfvvc vyaiigclsi arilainyn apmiiypais fletdnvtt
nvcvgkewyr ypstfflpdn srlkfvksef dgilpgefve snstwwnreg yyqiheimne
fnneetryt slescdflied lefdhskatv nepiysksdg wipvmvypfi dtkqtpfmg
afavpfiepk wgryeilvkk pvkidfsnlr raskqqa

Arabidopsis (SEQ ID NO: 12) (31.2 %)

mdltttrqrr plisdsssss stksysktdk pgrsnggdae dgglrwflpf ialcylryms
atsniihdcd evfnywepih yilyksgfqt weyssnfalr syllylfhel agrpaswwfg
ddkvrvfayv rlfglvsvs sdtvlvvals rkygkriaty avamlcltsg cffastsflp
ssfsmyaisl ssglllfeky amavavsvvg vilgwpsil aflpvviysl vkrfkqafia
gavttifilg vsllvdyyyy krwtssvlnl liynvlgge shlygtagal fyirngfnnf
nfcfilamlf vaiypvirrk ydrallvvis pmyiwlafms lqphkeerfl ypiyplivcs
asavienipe lfreyssre silvtitkym rpvilgcilc ashstfali ngysaplevy
kllchddag pgsvlcvgse whrypsffv phyisevrwi ddgfrglpfp pfnntlggts
aspyfnnkn qaseeqylkn ietctfliel qlsrpyqyrg sdlistweaia vlpdyldrels
pakyrffip hmqeknvfg kyvalrrvpk

C. elegans (SEQ ID NO: 13) (33.1%)

mvthrrkgs gppqkpppri vdrssfdadk kkikveklyh kannpdndwp fsfgsvfkm
lsirisgaiw giindcdevy nywepihlfl ygegfqtwey spvyairsyf yiylhyipas
lfanlfgdtk ivvftlirlt iglfcollgey yafdaickki niatgrffil fsifssgmfl
astafvpssf cmaiftyilg aylnenwtg ifcvafstmv gwpfsavlgp pivadmlllk
glrirfils lviglcigv qvitdshyfg ktvlaplnif lynvvsqpgp slygeepslf
yiknlfnwn ivifaapfgv plslayftkv wmsqdrnval yqrfapiill avttaawlli
fgsqahkeer flfpiypfia ffaalaldat nrlclkklgm dnlsilfil cfailsasrt
ysihnnysgsh veiyrslae ltnrtfnknf hdpirvcvgk ewhrfpssff ipqtvsdgk
vemrfiqsef rgllpkpflk scklvevtrh iptemnnlq eeisryvdld scdyvvdvdm
pqsdrepdfr kmrqnykrkt kkkwkriena ilqfwlnslf eeikflnsnf hsfpffffvd
nfglfqaysh ysflkitgnq wirfhssmsp nqqsmsgffv hfmfhsflpn ims

FIGURE 8

D. melanogaster (SEQ ID NO: 14) (40.6%)

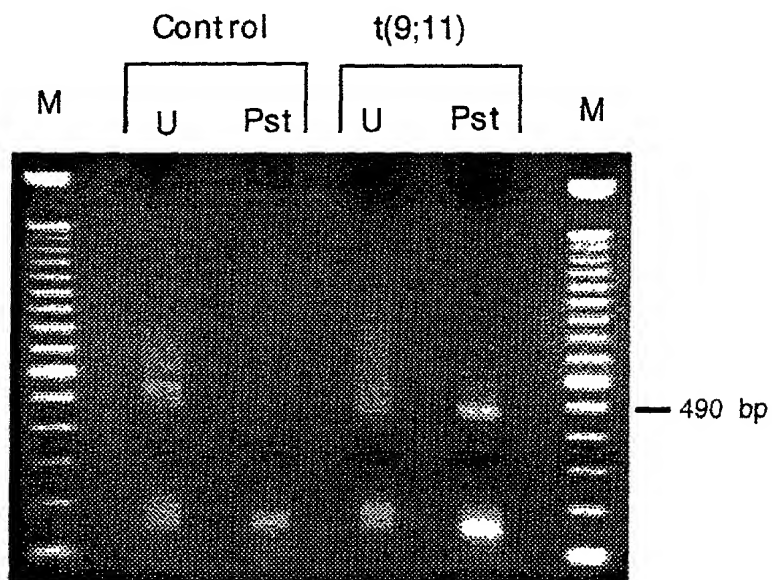
mappaarary iankadnqil skkppkrpgl ngnnktkeat pagkkkdka kkrnqptsgg
gekglpnpim psvqtafktf vsarlcasaiw ayiadcdetf nyweplyhyi nghglqtwey
spqfglrst ylllqgvpgy fyqklfnpsp ilifymvrcm lgfgcavmer ymysicqef
gihigrwlwli qqlfsvgmfv sstallpssf smyfgcaala awwqqnycfa ifltaisall
gwpfaaligi plvlemlrlq rdwktfvqwt lisgatvaip miaidtsyfg kltfaplniv
wynvftshgp nifgteplsy yiingflnfn iiwllalqlp imlvidyliv pakskstlnf
phyislaply lwllvffaqp hkeerflfpi yplislcgai tvdvyqriff rmksvvfkik
agvhyldhsm fiailmvmts tllglsvrfa lyrnyhapmd lmlelnqfka tpqydpdviy
nvcigkdwhr ypgsfffpak nfrlrflkse frgmipayyd egqnatkvvq pyfndlnqen
ehmyfdydrd dflvdfdegk ytalepnysk rskdwsvmks lpflipeksh kvlrafyvpf
ltdnhiqygd fnllkrktkr ngr

S. pombe (SEQ ID NO: 15) (33.1%)

mpskaprksl svsfvwtfsi lavlrlltsas frviddcdev ynyweplyhyi lygyglqtwe
yspeyairsw fyialhavpg flarglglslr lhvfyrirgv lacfsafcet nlilavarnf
nravalhlts vlfvnsgmws astsflpssf amnmvtlals aqlsppstkr tvkvvsfity
gavigwpfsa alsipfille lvdikgrfrh lfcwrfkaif vallitgici tvdslyfhyri
qfvawnivky nvlakdgrgp diygteppwy yfanlsiqhn ivlwfamagc plvllaafn
winldsflldl ssvispfyiw lfifiiqphk eerfmypiyp vlclaaagil dmslklmiqi
lssinetvrs kfpvrfrvvc vyaiigclsi arilaiqnyn apmiiypais fletdnvtt
nvcvgkewyr ypstfflpdn srlkfvksef dgilpgefve snstwnnreg yyqipehmane
fnneeptryt slescdflid lefdhskatv nepiysksdg wipvmvypfi dtkqtpfmg
afavpfiepk wgyeilvkk pvkidfsnlr raskqqa

FIGURE 8

The diagram illustrates the RT-PCR process for generating a fusion transcript. It begins with an mRNA template (3' end) and a fusion partner (5' end). Reverse transcriptase (RT) and dATP, TdT are used to synthesize a cDNA strand. The cDNA strand is then amplified by PCR cycles, followed by PST-1 digestion and re-amplification cycles. The final product is a fusion transcript.



Fusion Partner	pMT exon7-8boundary
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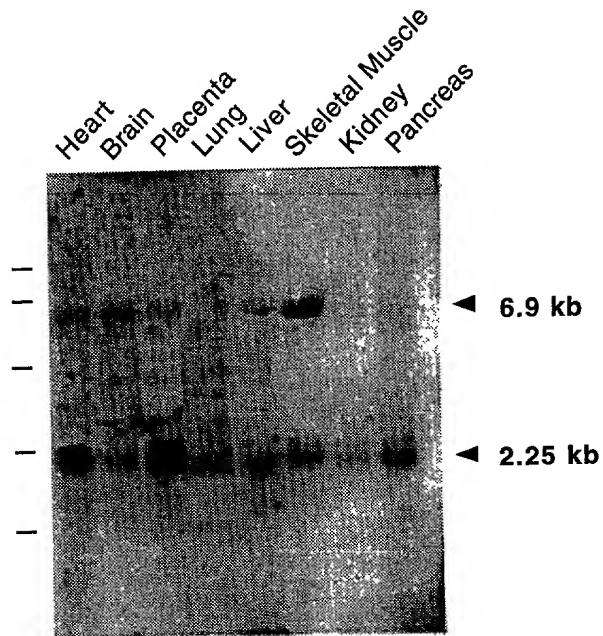
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FIGURE 9

Figure 5

Expression Studies

A



B

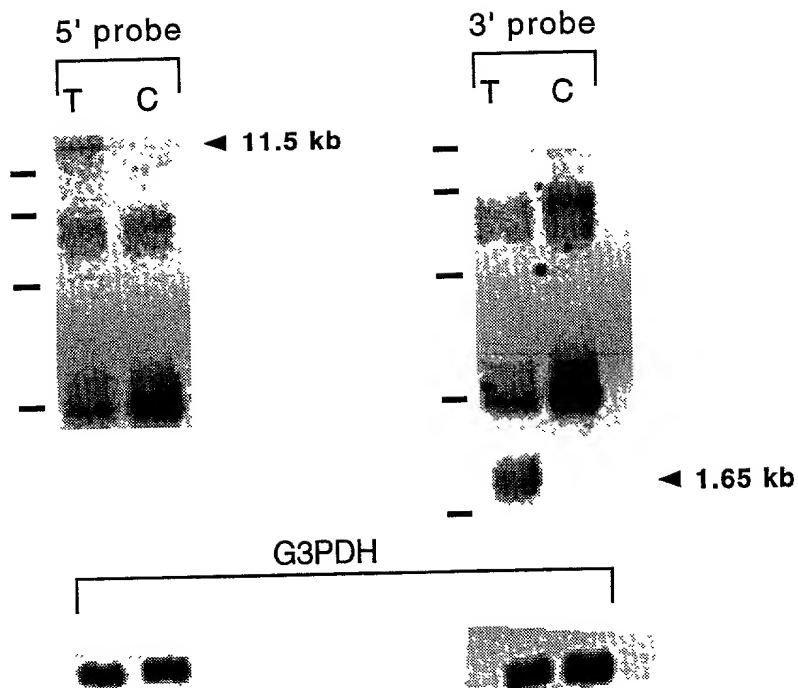


FIGURE 10